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RLDFWHSLGTWMVPELIRTFRAEHPNVEFQLHQAAMLLVDRVLADETDLALVGPKRA
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DALAEEAGFYDNYVPESMELTTVAGLYSAGLGYGYVPMDDPYLPTYGIYQRPLSPPAY
RELGLWRLMAGPAPAYDNPRKFYAGSRYALEEG"
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                                                                   Continuation (23 o
AL939107 Streptomy
AE017014 Bacillus
BX572598 Rhodopseu
Continuation (50 o
Continuation (50 o
AE017040 Bacillus
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AP006572 Gloeobact
AE017281 Bacillus
AP003007 Mesorhizo
Continuation (50 o
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Continuation (51 o
AP005050 Streptomy
AE011854 Xanthomon
AE004736 Pseudomon
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Continuation (38 o
BX64044 Bordetell
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
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    ^crganism="Corynebacterium glutamicum"
/mol type="unassigned DNA"
    ^db_xref="taxon:1718"

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Best Local Similarity 100.0%; Pred. No. 1e-211;
Matches 930; Conservative 0; Mismatches 0;
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Nucleotide sequences which code for
Patent: WO 0212504-A 1 14-FEB-2002,
Degussa AG (DE)
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AR271638 Sequence
AR564393 Sequence
AL939121 Streptomy
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Sequence 7069 from Patent EP1108790.
AX127153 AX114121
AX127153.1 GI:14041141
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Corynebacterium glutamicum Corynebacterium glutamicum

127764 128244 128184 128124 127944 127884 127824 128304 540 ö 480 099 240 360 9 sed 7069 128123 ACAATCCGACTGGACTTCATGCATTCCTTGGGCACTTGGATGGTCCCCGAACTTATCGGA 128063 ACATTCCGCGCCCGAACACCCCAACGTAGAATTCCAACTCCACCAAGGGGCAGCAATGCTC GAGGTTGGTACCTCTTTAGGGTGGCGCCACTGCTTCGTCAACGACTTGCCTAGCTGTT CCGCAGATCACCGGCTTGCCTTTTCTGGCCAAGGAGAATTGCCGTTGATTACTGCG TTAGCCGAAGAAGCCGGTTTTGTTCCCAATGTGGTTTTCGAATCCATGGAACTCACACC 128423 GTGACCATGGGCAACGGCGGGGAACCTGCGAATCGACGACCTACGCAGCTTCATTTCA CTTTCCAGACGAATCAGCCGAGTGGAAAACACGCAGCACCCCCACTTTTCGACCGCGCC CTTTCCAGACGAATCAGCCGAGTGGAAAAACACGCAGGGACCCCCACTTTTCGACCGCGCC 128243 GGCCGCAAACTCGTCCTCAACCAAGGCCACGCCTTCCTCAACCACGCCAGCGCCATC GTCGCAGAATTCAACTCCGCCGCAACTGAAATCAAACGCCTCATGGACCCAGAAAAGGC ACAATCCGACTGGACTTCATGCATTCCTTGGGCACTTGGATGGTCCCCGAACTTATCCGA CCCGCAGATCACCGGCTTGCCTCCTTTCTGGCCAAGGAGAATTGCCGTTGATTACTGCG GCGGAAGAACCTTTCGTGGGGATGCGAGCAGGTTTCGGCACCCGACTCCTCATGGATGCA TTAGCCGAAGAAGCCGGTTTTGTTCCCAATGTGGTTTTTCGAATCCATGGAACTCACCACC GTCGCTCAATCAGGCCACCTCACCGAAACTGCCGAAAGATTAGGCATCCCGCAGCCCACA GGCCGCAAACTCGTCCTCAACCAACGAGGCCACGCCTTCCTCAACCACGCCAGCGCCATC ACATTCCGCGCGCAACACCCCAACGTAGAATTCCAACTCCAAGCGGCAGCAATGCTC CTGGTAGATCGTGTTTTGGCTGATGAAACTGACCTCGCATTAGTTGGCCCCCAAACCTGCC GAGGITGGIACCICITIAGGGIGGCGCCACIGCITCGICAACGACITGCCCTAGCIGIT 1 GIGACCAIGGCCAACGACGCCGGAGACCIGCGAAICGACGACCIACGCAGCTICATITCA Gaps Nakagawa,S., Mizoguchi,H., Ando,S., Hayashi,M., Ochiai,K.,
Yokoi,H., Tateishi,N., Senoh,A., Ikeda,M. and Ozaki,A.
Novel polynucleotides
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Novel polynucleotides
Novel polynucleotides
Novel polynucleotides
Novel polynes genomic DNA"
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3.000.001 3.309.400 309.400" Length 309400; ö Indels ; Score 930; DB 6; L ; Pred. No. 8.9e-212; 0; Mismatches 0; 127703 g

δ 셤 8 셤 8 유 ACCESSION VERSION KEYWORDS SOURCE

LOCUS

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                                                                                                                                                                                                              TESQEMGKAIYEADAAAGATQADAGAEGAADDNVVDAEVVEDDAADNGEDKK"
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Corynebacterium glutamicum ATCC 13032 DNA, complete genome, section
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                                                                                                                        900
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Unpublished
2 (bases 1 to 325651)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (24-MAY-2002) Satoshi Nakagawa, Kyowa Hakko Kogyo Co.
Lid., Tokyo Research Labbratories, 3-6-6, Asahi-machi, Machida,
Tokyo 194-8533, Japan (E-mail:snakagawa@xanagen.com,
Tel:81-44-829-3031, Fax:81-44-813-1651)
This sequence is conducted by collaboration of Kyowa Hakko Kogyo
Co. Ltd. And Kitasato University.
Location/Qualifiers
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Corynebacterium glutamicum ATCC 13032
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Corynebacterineae, Corynebacteriaceae, Corynebacterium.
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Direct Submission
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781
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AP005283/c
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AUTHORS
TITLE
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AUTHORS
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CDS

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FEATURES COMMENT

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FIGHER TREATMENT OF THE TRE
DRAREMETLAHDNVKQI VGAQHGI LSAKREGAVDKRRTI STARAGLDALVKGLGGAAP
ESAEELLELNNAARLI VDEY PAAREALESAGQRNVEDRTRAVDEFKAADQELSSLSKG
SSNI EYRLLQVRENLCQDLGVSPRDMPFAGELI DPNNAEWEPVVQRI LIGGFAAEMLVP
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AARAARGEGTYSLININDTPLVRIGHDVRSIAGLKLKANGEBERVEDLPEVVEGGELDT
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Gaps

Query Match 100.0%; Score 930; DB 1; Length 325651; Best Local Similarity 100.0%; Pred. No. 8.9e-212; Matches 930; Conservative 0; Mismatches 0; Indels 0;

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BX927156 BX927147
BX927156.1 GI:41326831
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              144674 GTGACCATGGGCAAGGACGGCGGAGACCTGCGAATCGACGACCTACGCAGCTTCATTTCA
                                                                    144614 GTCGCTCAATCAGGCCACCTCACCGAAACTGCCGAAAGATTAGGCATCCCGCAGCAA
                                                                                                                                                                                      144494 GGCCGCAAACTCGTCCTCAACCAACGAGGCCACGCCTTCCTCAACCACGCCCATC
                                                                                                                                                                                                                                          144434 GTCGCAGAATTCAACTCCGCCGCAACTGAAATCAAACGCCTCATGGACCCAGAAAAAGGC
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                                                                                                                            144554 CITICCAGACGAATCAGCCGAGTGGAAAAACAGGCAGGCACCCCACTITTCGACCGCGCC
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Bielefeld University.

BX927150.151. 348475,

BX927151.151. 348475,

BX927151.151. 348475,

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Location/Qualifiers
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ALASALPSADATSLDIKLRDGATFHNGDAVTADDVVSSFERVLDPANNSLYASFIPFI
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TDSRMWKGSESYDVQVOLLEEGIRATDKAEQQDIWNTFTPVISDNVBLYPLFHRKVY
TAMNSNALVDFKPISLTGLNFSGVATTE"
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/transl_table=11
/product="ABC-type dipeptide/oligopeptide/nickel transport
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SSPERLEARYREANGLNDPMYNRYPEPTIGM: SSSPERLEARGYNAVTDIVARAPFITLO
LITEMGLIIAVVVALLIGVIAALYRDRWPDQLIRVVSIAALATPSFMLAILLIGVIAALYPENGT
PGAWGFPPALVTRWVPFSEDPATYFNNIALPALAVPVAGSLARVVRTSMVEBLUKD
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E-mail:Joern.Kalinowski@Cebitec.Uni-Bielefeld.DE
                        Corynebacterium glutamicum ATCC 13032
Corynebacterium glutamicum ATCC 13032
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="genomic DNA"
/strain="DSM 20300 = ATCC 13032"
/db_xref="taxon:196627"
/note="IS_fingerprint type: 4-5"
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/protein_id="CAF20677.1"
/db_xref="GI:41326833"
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307. .1917
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JP 2002191370-A/3228
09-JUL-2002
15-DEC-2000 JP 2000405096
SATOSHI NAKAGAWA, HIROSHI MIZOGUCHI, SEIKO ANDO, MIKIO HAYASHI,
                                                        307844 ACAATCCGACTGGACTTCATGCATTCCTTGGGCACTTGGATGGTCCCCGAACTTATACCGA
                                                                                                                                                                  307784 ACATTCCGCGCCGAACACCCCAACGTAGAATTCCAACTCCACCAAGCGGCAGCAATGCTC
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                          ACAATCCGACTGGACTTCATGCATTCCTTGGGCACTTGGATGGTCCCCGAACTTATCCGA
                                                                                                                                       ACATTCCGCCCCGACCCCCAACGTAGAATTCCAACTCCACCAAGCGCCACAATGCTC
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Nakagawa, S., Mizoguchi, H., Ando, S., Hayashi, M., Ochiai, K., Yokoi, H., Tataishi, N., Senoo, A., Ikeda, M. and Ozaki, A.
Novel polynucleotide
Patent: JP 2002191370-A 3228 09-JUL-2002;
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/Jouns tage reg-
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/Locus tion="MTMSTIPNGIATDAHQIEAGKPCMIACLLFEGVDGCEGHSDGD
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LSGFLALYKDFHKSPKRK"
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'db_xref="GI:41326838"
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/transl_table=11
CYTIDYLYLTRANS"
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/locus_tag="cg2946"
                                                                                                                                                                     /locus_tag="cg2944"
complement(7624..8106)
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complement(8099. .8869)
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/EC_number="2.7.7.-"
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Matches 930; Conservative
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
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Yokoi,H., Tateishi,N., Senoh,A., Ikeda,M. and Ozaki,A.
Novel polynucleotides
Patent: EP 197990-A 3282 20-JUN-2001;
KYOWA HAKKO KOGYO CO., LTD. (JP)
Location/Qualifiers
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/organism="Corynebacterium glutamicum"
/mol type="unassigned DNA"
/db_xref="taxon:1718"
                                                                                                                                                                                                                                                                                                                                                                                                 AX123312 924 bp DNA Sequence 3228 from Patent EP1108790. AX123312
                                                                                                                                                                                                                                TCGAGGTATGCATTAGAAGAGGGC 930
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PC 04,C12P13/08,

G01N33/59,00,C12P19/34,C12P21/02,C12Q1/37,C12Q1/68,G01N33/53, PC

G01N33/569,G01N33/68,G01N37/00//C12P21/08,(C12N1/21,C12R1:15),

PC (C12N1/21,C12R1:13),(C12N1/21,C12R1:01),(C12P13/08,C12R1:15),

PC (C12N1/21),C12N15/00

PC (C12NS)O0,C12N15/00

CC Novel polynucleotide

FH Key Location/Qualifiers

FT Source Location/Qualifiers

FT Source Location/Openity (C12N1/21),C12R1:15),

PT Source Location/Openity (C12N1/21),C12R1:15),

PT Source Location/Openity (C12N1/21),C12R1:15),

Corpus (C12N1/21),C12R1:15),

PT Source Location/Openity (C12N1/21),C12R1:15),

C12N1/21,C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),C12R1:15),
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    .924
    /organism="unidentified"

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/db_xref="taxon:32644"
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Kawarabayasi,Y., Yamazaki,J., Hino,Y., Kikuchi,H. and Director-General of Biotechnology Center.

Direct Submission

Submitted (17-MAY-2002) Director-General of Biotechnology Center, Direct Submission

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Nishio, Y., Usuda, Y. and Sugimoto, S. are at the Ajinomoto Co., The other authors are at the National Institute of Technology and Evaluation, Shibuya-ku, Tokyo, 151-0066 Japan.
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complement(52. .1248)
/note="CE2590, similar to X89084-2|CAA61456.1| percent
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                           CTGCCCGAGGTTACCTCTTTAGGGTGGGCGCCACTGCTTCGTCAACGACTTGCCCTAG
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  TGCTCCTGGTAGATCGTGTTTTGGCTGATGAAACTGACCTCGCATTAGTTGGCCCCAAAC
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Corynebacterium efficiens YS-314 DNA, complete genome, section
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Corynebacterium efficiens YS-314
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/strain="YS-314"
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                             GGTACCTCTTTAGGGTGGGCGCCACTGCTTCGTCAACGACTTGCCCTAGCTGTTCCCGCA
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    GGTACCTCTTTAGGGTGGGCGCCACTGCTTCGTCAACGACTTGCCCCTAGCTGTTCCCGCA
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Corynebacterium glutamicum
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Corynebacterineae, Corynebacteriaceae, Corynebacterium.
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|mol type="unassigned DNA"
|db xref="taxon:1718"
|noFe="lysR2int"
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Best Local Similarity
Matches 439; Conserv
    487
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SOURCE
ORGANISM
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ACCESSION
VERSION
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AX376729
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/product="adenylosuccinate synthetase"
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/protein_id="macly407.1"
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/protein_id="macly
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VTVVAREISPPPGVVTVGALNAGTFANIIPESBEZILVMTRAMSVBIGERKIRTAIERI
VTSECEAAGCPAEPFEYDRAPITFNDADARSVVALAFNQARGERVQVTPESTASED
FSVIPDALGVPYVFWFVGGYEDPENAPGNHSPFFAPVIQPTLDRSLEAFITAASAMLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /trānslation="WKTPRPRLPLPKVPVKVSGMRAVTGAPAGTFAEPRWEKARGTLH
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BFCVAAPELDCWKDARILEYHAATSHLISSAAALIGARFDDNSPPPAIDTAMAFDAVF
TKLGTAPHEDTRSRFYTRMSPRDIMDALSHFEYRPY"
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BLNRDDSTTNQP"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /trānslation="Myaetlehttrpraefrhrntkvvhmrlvvlrcaapsftdepga
pvapevhdlpevptrrdlrmlddaafdvlphdptpsldelarqpdvahlgtpqpapqh
peqplrlvvlgsdaslsavltrlmradnmmaevayvptgesvaaknwglpadpgaalr
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GIFGARLVPMMVAPGIAAAVMDTPAPGTEIKKGLFRRPTGTLIPESLSTGRATQAGGP
SLRVTVDGVSRKRAVERVTFYRHLRDLQVVRP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NMDIDKLIDVTATGAVAIIENCDGPVVALRGDIDALPVTEQTGLDYASEAHGVMHACG
HDFHITTLLSAVDVFASNRDKWSGTLVAVFQPAEETASGARAMVEADIASVIPKPDVY
LENARSVAAR I TNALGGRGVFGVELFVSGDDVY FSEVSPRPHDTGLVTLATQRFSEFE
LHAKAVLGLPVDVTLTSPGASAV I YGGVDSPGVSYAGLAEALAVABTDVRLFGKPEAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /EC number="6.3.4.4"
/note="CE2597, similar to AL583918-8|CAC29788.1| percent
identity: 61 in 429 aa"
                                                                                                                                          :584. .7768
note="CE2595, similar to AX064083-1|CAC25282.1| percent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10063. .10989
/note="CE5598, similar to U23181-6|AAC48204.1| percent
identity: 20 in 247 aa"
/codon starte!
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="conserved hypothetical protein"
/protein_id="BAC19408.1"
/db_xref="GI:23494442"
                                                                                       FKRRMGVAVSTAEDTATARDRATLAAAAVTVHG"
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/protein_id="BAC19406.1"
/db_xref="G1:23494440"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (8727. .10016)
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                                                                                                                                                                                                                   in 391 aa"
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/note="CE2596"
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/transl_table=1
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/note="CE2599"
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                                                                                                                                                                                                                   dentity: 38
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                                                                                                                                                                     /protein_id="BAC19400.1"
/db_xref="GI:23494434"
/translation="MALALVINSGSSSIKFQLVNPANHATDDPFVSGLVEQIGEKMGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DKLKKAVRNHGNLEPVMSAALFENWLLKRARKEQAHIVLPEGEDDRILMAAHQLLEKD
ICELTILGDPEQIHSRATELGLHLEKADVINPLTDPKLDEFAEGFAELRKSKGITLEQ
ARETMKDISYFGTMMVHNGDADGMVSGAANTTAHTIKPSFQIIKTVPEASVVSSIFLM
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DLAMESHDHOVDIDFRENDAPFGLIRVKVGAPDHPRIKGIVKSHHNVDVENGEQLRILGNI
BIGKNITVDELREFYGATIFSTGATGDQDLRYKGADLEGSWGAGEFVGFYDGNPDFAR
SWDLSAEKVAVIGVGNVALDVARILAKTGDELKVTEIPDNVYESLSQNKAREVHVFGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RGPAQAKFTPLELKELDHSPNIEVVVNPEDIDYDAASEQARRDSKSQDLVCQTLEQYA
INDPKAAPHTALFIHFESPVEILGEDGKVVGLKTERRILDGNGGVVGTOGEFTHWDVQA
VRANGYRSDAVRDVFDDERAI IPNDGGRV DPSTGSPVTSLYATGNIKRGFIGLIG
NTKSDAKETTEMLLADYAAGSLPAPANPETDAIIELLDDRKIPYTTWDGHHLLDAAER
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TDALPTTRHIIWWERHEDHPTELKGCARLVPTTVSEVAAATGATLELDDAEVSQLGRV
AVSQDSRGTGLSAEIMENALRLAYEQFPGKDVVLTAQLPLQEFYEGFGFTTCGTQYDE
AGVAHVPMVLKASELVRYAA"
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DFI I PEI EALATDELVR I EQEGLATVVPTARATQLTMNREG I RRLASSEELGL PTSGYE
FCSTFEEFTAAAERLGY PNVVKPVMSSSGKGQSVVTSAEDLESAWEYAMSGARVSNOR
                                                                                                                                                                                                                                                                                                           IILKI EGEKVVKEAPIADHSAGLSMSFDLMTEHGCGPSQVDIIAVGHRVVHGGILFSA
PELITDBIVEMIRDLIPLAPLHNPANIDGIEVARRILPDVPHVAVFDTGFFHSLPPAA
                                                                                                                                                                                                                                                                                                                                                                                                   ALYAINKDVAAEYGIRRYGFHGTSHEYVSSRVVDLMDKPAEEINTITFHLGNGASMAA
                                                                                                                                                                                                                                                                                                                                                                                                                                            VKGGVAVDTSMGMTPLAGLVMGTRTGDIDPGVVFHLARNANMSIDEIDNLMNKKSGVK
GLSGVNDFRELHQMIEDGDQDAWSAYNIYIHQLRRYLGSYMVALGRVDCLVFTAGVGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     translation="MRYRASNDAKLCEESQHLPRVPSGTHLVERITPISSGLREERRC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MSDTPTSALITTVNRSFDGFDLEALARDLEVNLVPIRGDDFDMSKVLAADLLADGPAL
IVGAGNAHFDAQVAAALGVPMLMLVDKRGSHVTLARTQAKNVGAVVVAAFTAEEEAKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VLRGRLWAFGDCAVNPNPTAEQLGEIAVVSAKTASQFGIDPRVAILSYSTGNSGTGPD
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identity: 42 in 465 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(1252. .2766)
/note="CE2591, similar to AE006946-9|AAK44645.1| percent
identity: 45 in 495 aa"
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/note="CE2594, similar to AX064627-1|CAC25553.1| percent
identity: 86 in 401 aa"
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/protein_id="BAC19402.1"
/db_xref="GI:23494436"
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/transl_table=11
/product="putative_phosphoribosylglycinamide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="phosphate acetyltransferase"
/protein_id="BAC19401.1"
/db_xref="GI:23494435"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="hypothetical protein"
/protein_id="BAC19403.1"
/db_xref="GI:23494437"
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                                                                                                                            /product="acetate kinase"
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/db_xref="GI:23494438"
identity: 85 in 397 aa"
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/transl_table=11
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/transl_table=11
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/note="CE2593"
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/transl_table=
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WPCOMMENT
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AF116907.2 GI:10657865
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A physical map of the 85 kb virulence plasmid
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Corynebacterineae; Nocardiaceae; Rhodococcus.
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Zheng,H., Tkachuk-Saad,O. and Prescott,J.F.
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Direct Submission
Submitted (29-DEC-1998) Veterinary Microbiology and Pathology,
Washington State University, PO Box 647040, Pullman, WA 99164-7040,
USA
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375 ACACCCCAACGTAGAATTCCAACTCCACGAGCGGCAGCAATGCTCCTGGTAGATCGTGT
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Corynebacterineae; Nocardiaceae; Rhodococcus
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Unpublished
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/note="fragment d"
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/mol_type="genomic DNA"
/strain="103"
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VYBAINQPSESAIBANLARGEIDVAYLGRPRAABEDFWYELVERLCHAVPESHELAG
RATIRIADASDNAFTHRRPPGELKLVDELPAAGGVVPQIVFETIEIPTLEGLVAAGF
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GATILGAGVRHNLLGRTLCDIFNSRLGGFHNSCDDKAGLVDALEASFEEVDVAVEGST
AKFIARRPHSEPDESPRTLTSVGSDLLVCPGQL"
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GVGRRPVLLGGTGAIFLGGAYTLASNIMILVCGLVLYTAGFFGAHSVVSGWVGAEVSA
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Ontario, WA NIG 2W1, Canada
Sequence update by submitter
On or before Oct 5, 2000 this sequence version replaced gi:4713919,
gi:4680487, gi:4325102, gi:3834551, gi:3834552, gi:4680486.
Location/Qualifiers
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DNA sequence and comparison of virulence plasmids from Rhodococcus equi ATCC 33701 and 103
Infect. Immun. 68 (12), 6840-6847 (2000)
Development of a Rhodococcus equi-Escherichia coli plasmid shuttle
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Zheng, H. and Prescott, J.F.
Direct Submission
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NA sequence and comparison of virulence plasmids from Rhodococcus equi ATCC 33701 and 103

Infect. Immun. 68 (12), 6840-6847 (2000)
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                                                      5423 ACGTAGÁACGCCTTTGCCTCGCTGTGCCGGAATCTCACC-------CCTTAGCGGGGC
TTCGTCAACGACTTGCCCTAGCTGTTCCCGCAGATCACCGGCTTGCCTCCTTTTCTGGCC
                                                                                                                                                                                 5474 Gréceacrarcégéarageagacécrrécéaraacecrirécarrarécrecécagecear
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Corynebacterineae, Nocardiaceae, Rhodococcus.
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Takai,S., Sekizaki,T., Kakuda,T., Nakamura,M., Suzuki,K.
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Rhodococcus equi plasmid pREAT701 DNA, complete genome.
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/gene="orf64"
complement (join(80267. .80610,1. .184))
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10963. 11122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5008
                                                                                                                                                                                                                                                                                                                                                                /tränslation="MESIRGISVILADRDPALRTATRRVFEQLGMVVREAGNGDEVLR
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MITLTSREFDLLAYFMKNPFVIHSRQDLLERVWKWSYGDLSTUTVHVRRLRKRLGNYS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ~
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5189 CTGCGCTCCGTAATCCTGAGTCAGGCACCGTTCGGCTAGGCTTCCTGCACTCCCTTGCGA 5248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5249 GIIGGIIIGIGCCIGAGAICAICCGGGIGIIICGCGAGAGCGCGCCGAGGGIGAACIICG 5308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5309 CGCTGAACCAGGCTCCGAGCGAGGCCATCGAAGCGATGCTGGCTCGGGGGGAGATTGATG 5368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           395 AACTCCACCAAGCGGCAGCAATGCTCCTGGTAGATCGTGTTTTGGCTGATGAAACTGACC 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCGCATTAGTTGGCCCCAAACCTGCCGAGGTTGGTACCTCTTTAGGGTGGGCGCCACTGC 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAAGATTAGGCATCCCGCAGCCCACACTTTCCAGACGAATCAGCCGAGTGGAAAAACACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35 TCGACGACCTACGCAGCTTCATTTCAGTCGCTCAATCAGGCCACCTCACCGAAACTGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4949 treaceaacrecerecrirerececerraceaarcecacacacacececere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 215 CCTTCCTCAACCACGCCAGCGCCATCGTCGCAGAATTCAACTCCGCCGCAACTGAAATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            275 AACGCCTCATGGACCCAGAAAAGGCACAATCCGACTGGACTTCATGCATTCCTTGGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14.3%; Score 132.8; DB 1; Length 80609; larity 51.1%; Pred. No. 5.2e-21; Conservative 0; Mismaţches 342; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10574. .10759
/note="ORF 10; part of pathogenicity island"
                                                                                                                                          8534. .9292
/note="ORF 8; part of pathogenicity island"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10278. .10505
/note="ORF 9; part of pathogenicity island"
/codon_start=1
/trans___table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RIETVWGRGYRWIPGPPVPQVAASSDERLAGPRH"
10278. .10505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     product="unknown"
                                                                                                                                                                                                              codon_start=1/
transl_table=11
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Best Local Similarity
Matches 373; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95
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                                                                                 / translation="MindGvPVTAITYARELLPTKYTARAAGFFVGGAAVGGWACRLIS
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AWGARPVLLFGTGA FTLGGAVTLASNLWILVCGLVLVTAGFFCAHSSVSGWVGBVSA
GTRASSIYTLAYYGGASLFGWLGGSAYZSYSWPGLVATGFFCAHSVVSGWVGBVSA
SAAEIVRQDWQVEAVQEGNDNAVACP"
7367. 7930
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_gtart=1
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PTWREEGANYSDGTWLVRASSNFLEPSTHSDSGQQQWTVQGVLASALVYQRLKLNVBG
GETFEGYAGGLSFPGGAMVWGTLFTDNIQRLYDRTESFEFNAVGPYLNVNFFDGHSAI
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10278. .10505
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7982. .8419
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/gene="tcr"
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/gene="orf4"
4993. .5829
/gene="orf4"
4995. .5829
/gene="orf4"
/note="similar to Bacillus subtilis LysR family of
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in 273 aa overlap); DAD:d26185-26"
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/transl table=11
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/product="tanscriptional regulator"
/product="tanscriptional regulator"
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LATRVCIGSVMAPIAPSMGYFDSIAASPVFHRLPGTWSEKRLAIRHISHALKEDGVFF
GATILGAGVRHALLGSTRLCDIFNSRLGGFHNSCDDKAGLVDALBASFEEVDVAVEGST
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/gene="orffs"
/note="similar to Bscherichia coli Bicyclomycin resistance
protein(417 as) 2.6e-34(38.246% identity in 285 as
overlap); DAD:d90802-10"
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NAERFRKDLEKWIAAAAKVDGRPNRSKRSRMGSGGSRTSKEGLAAIRNWAADNGYHVS
TRGRIAREIVEAFEAAH"
complement (1541. .2059)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /transT_table=11
/poduct=n. equi VapG protein"
/product=n. equi VapG protein"
/protein id="Bab16611.1"
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SIPGVAVLEGTILFTEDLQHLYSDIVSFEYNAVGPFYLNINFFDSHGTLLGHVQSGSIGT
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Rimlehtrrslttelsagerlalandersgyvrlgfhislaswydelirvrrssapr
Vnfalnqaerbaleamlargeidvavigrpaadefdwyelyverlclavpeshplag
Ratiriadasdnaftmirrpfclirkuvdelpraagvvpqivpetieiptleglyaage
Gvavvpsprptketegvryvplddvgaprpiglampvgrepspvvtrflaflaplanrgqe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="similar to Rhodococcus equi virulence-associated 15-17kDa antigen(189 aa) 4.7e-23(47.541% identity in 183 aa overlap); PIR:jc4072" /codon start=1/transI_table=11
795. .1154
/gene="lst2"
/note="similar to Mycobacterium tuberculosis Lsr2
protein(112 aa) 1.9e-15(47.934% identity in 121 aa
everlap); DAD:z95557-4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /genes"orf3"
hote="similar to Escherichia coli hypothetical
protein(143 aa) 2.2e-12(42.478% identity in 113 aa
overlap) ; DAD:u82598-30"
                                                                                                                                                                                                product="Lar2 protein precursor"
protein id="BAB16610.1"
/db xref="G1:10801056"
                                                                                                                                                                                                                                                                                                                                                                                                                              complement (1541. .2059)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (3951. .4706)
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                                                                                                                                               /codon_start=1
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6322. .7230
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="vapg"
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DVAPRVAQIRGVDAVPTVVALAAGQPISSFQGMQPADQLRGWLDQILSATAGKLKGAT
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PDVLFLSEAFTPPVRQNGLTKLGFTQSYTYFTWRTAKWELTEFGNDIAALADFRRPNL
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GIGVIVDWVPAHFPKDAWALGRFDGTPLYEHSDPKRGEQLDWGTYVFDFGRREVRNFL
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TAHKSAPGIVTIAEESTSWPGVTRPTNLGGLGFSMKWNMGWMHDTLDYISRDPIYRSY
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FDPATGDCVLVVVTLNAFGPEEATLFLDMAALGMEPYERFWVRDEITGGEFQMGQANY
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LIGEFNGWTGTEAPMRVLGSSGVWELFWPDFPIGGLYKFKVHGADGVVTERADFMAFA
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                  avium complex (MAC).

1 (bases 1 to 302325)

1. (bases 1 to 302325)

1. (bases 2 to 302325)

Dir.L., Bannantino,J., Zhang,Q., Amonsin,A., Alt,D. and Kapur,V.

Direct Submission

Submitted (05-SEP-2003) Biomedical Genomics Center, University of Minnesota, 1971 Commonwealth Ave., St. Paul, MN 55108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KPLSLPMTMGPEPYVFHGQFTPDQVGLWTFRVDGWGDPIHSWRHGLVAKLDAGQGET
LSNDLLVGAELFERAATGVPRARREPLLAAAAALRTAGDPVTRTALALAPEIEEILA
  Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
                                                                                                                                                                                                                             organism="Mycobacterium avium subsp. paratuberculosis"
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complement (4550.5461)
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/codon start=1
/transI_table=11
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/protein_id="AAS04752.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sub species="paratuberculosis"
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                                                                                                                                                                                                                                                  str. k10"
/mol type="genomic DNA"
/strain="k10"
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329. .4524
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                                                                                                                                                                         Location/Qualifiers
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/locus te.
.2294
                                                 REFERENCE
AUTHORS
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10963. .11325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     575 AAGGAGAATTGCCGTTGATTACTGCGGCGGAAGAACCTTTCGTGGCGATGCGAGGTT
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Mycobacterium avium subsp. paratuberculosis str. k10
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                            Length 80610;
                                                                                                                                                                              15;
                                                                                                                                                                           0; Mismatches 342; Indels
                                                                                                                            DB 1;
                                                                                                                          Score 132.8; DB 1
Pred. No. 5.2e-21;
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51.1%;
                                                                                                                                                                           Matches 373; Conservative
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YGLVDTWFIPRELFGVSFCGVLVATACYLLAEFALRPVAAQALEAGPPPRRLTAGIMG
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                                                                    complement (5652. .6821)
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12082 regeceacecereceáracegareresecéarececerececeacarecegeridee 12141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QALLPALSAHYRI GPATAALTVSLTTGALALSI I PASVLSERYGRI RVML I SGVASSY UGLLLFRSPSESSYGYLAGAGGVALAGA PAVVAMALLAERVDASSLGSAMGYL TAGTTI GGLLAGRI UVBSVVQVGTWRVALLAGSLI TLAGTAVRAVLARTRI GGLAGRI UVBSVVQTWRVALLAGSLI TLAGTAVRAVLARTRI NLAGHLRNPVLAKLFAVGFVLMGGFVTVYNYLGYRLAARFFGLAPSVVGLLFLLYLVGTSVVAGRLADRRGRELLAGAALF TAVAGLLLTVPATLAALVRGVVFTGGFFAAHT VASGWYGAVAQDRAREASALLYLFSYYLGGSVAGAFGGGWLAGGWSTTGGFFAAHT GAALVALLVRONDRAREASALYLFSYYLGGSVAGAFGGGWLAGWSTVCFVVVLLMA GAALVALLVRNOGFRIGRRVATSVASVK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11902 chicarchicececececicandenacricentecriceinenicanicaricaricanicanicani
GRHVGREVALAAERERPKLGGEERHVAVVF1D1VGSTQLVTRRPPAEVVSVLNQPFG1
VVEEVDRHCGLVNKFEGDATLA1FCAPNHLDCPEDAALTAARA1ADRLANEMPQCRAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 136 AGCCGAGTGGAAAACACGCAGGCACCCCACTTTTCGACCGCGCGGCCGCAAACTCGTC 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                316 ITCATGCATTCCTTGGGCACTTGGATGGTCCCCGAACTTATCCGAACATTCCGCGCCGAA 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GACGGCGGAGACCTGCGAATCGACGACCTACGCAGCTTCATTTTCAGTCGCTCAATCAGGC 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTCAACCAACGAGGCCACGCCTTCCTCAACCACGCCCAGGCCCATCGTCGCAGAATTCAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.0%; Score 130.2; DB 1; Length 302325; 48.5%; Pred. No. 2.1e-20;
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complement (10525. .11787)

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complement (10525. .11787)

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11854. .12738
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Best Local Similarity
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LGAALLGAPPAHAAGLAKGUTKADITENDEN GUNNYERRALDAYAN TA GAALLGAALLGAALLGAALLGAALLGAALGAARGARGARGATKADITENDEN GUNNYERRALDAYAN TA GAALLGAALGAALGAARGARGAN TA GAALGAAGAAN TA GAATTA SUNNAN KERWATYAN TA GADAGAYAGLIS FADRYGFILV PABETTS SUNNAN KERWAYAGLAF GAATTAN SAALCHWACTDITAADOWARRYRDGTS WASCPWRYA I WHGOKOTTTA PRAND ELRDOWTA A WHGOKOTTTA PRAND ELRDOWTA A WHGOKOTTOTTA PROND ELRDOWTA A WHGOKOTTOTTA SAND TA GAAD FELDSI CSSYWITOF PREGESCAS AD SEGLES AND EGLES AND TA GAATTA TA GATTA TA TA GATTA CATTA TA TA GATTA TA TA GATTA A TA GATTA TA KERWA GATTA A WAGAGA TA TA SAGYTYAKGS GONNGI YNTFVITIKES PT
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complement (2020. .3579)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="transcription regulator"
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                                                                                 protein_id="AAF86380.1"
db_xref="G1:9280382"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="AAF86382.1"
/db_xref="GI:9280384"
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/db_xref="GI:9280385"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (2020. .3579)
/gene="fkbU"
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/gene="fkbR2"
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/transl_table=11
/product="FkbR1"
   codon_start=1
/transl_table=11
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/transl_table=11
/product="FkbB"
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                                                               product="FkbW"
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/transl_table=:
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                                                                                                                                                                                                                                                                                                                                                                                                                                      gene="fkbu"
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/gene="fkbE"
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gene="fkbE"
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                                                   12262 CGGTCCGGCGCGTGGACATCGGGGTGGTATCCCCGCGACCGGTCGAG-----CGAACC 12315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12427 GTGACGATGCACCCCGGTTTCGGGATGCGACGCTCCTCGACGACGACTTTGCGCCGCAGCC 12486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12487 CAATTCCGGCCTCGGGTCGCCCTGCAAGCGCCGAATCTCACGACCGCCGCCCACCTAGTC 12546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12547 GCCGCGGGGCTGGGCATCAGCCTGGTCCCGATCGACGGCAGCTATCCGTCGGGAGTA 12606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptomyces hygroscopicus var. ascomyceticus FK520 biosynthetic gene cluster, partial sequence.
AF235504.1 GI:9280381
                                                                                                                                                                                                                                  555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  675
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Reeves,C.D., Wu,K., Chung,L., Revill,P. and Katz,L.
Direct Submission
Submitted (16-FEB-2000) Kosan Biosciences Inc, 3832 Bay Center
Place, Hayward, CA 94545, USA
Location/Qualifiers
376 CACCCCAACGTAGAATTCCAACTCCAAGCGGCAGCAATGCTCCTGGTAGATCGTGTT
                                                                                                            436 TIGGCIGATGAAACTGACCTCGCATTAGTTGGCCCCCAAACCTGCCGAGGTTGGTACCTCT
                                                                                                                                                                                                                               496 TTAGGGTGGGCGCCACTGCTTCGTCAACGACTTGCCCTAGCTGTTCCCGCAGATCACCGG
                                                                                                                                                                                                                                                                                                                                               556 CTTGCCTCTTTTCTGGCCAAGGAGAATTGCCGTTGATTACTGCGGGGAAGAACCTTTC
                                                                                                                                                                                                                                                                                                                                                                                                        12376 TTCGCC-----CGCGGTGCCGCGGTGTCCATGGTGGACCTGGCCGACGACGACCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTGGCGATGCGAGGTTTCGGCACCCCGACTCCTCATGGATGCATTAGCCGGAAGAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              676 GGTTTTGTTCCCAATGTGGTTTTCGAATCCATGGAACTCACCACCGTCGCAGGGCTTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 736 AGCGCAGGTCTCGGCGTTGGTGGTTCCGATGATGCATGCTCCGTACCTTCCCACAGTGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    796 ATCGTGCAACGCCCACTTAGTCCACCGCTTATAGGGAACTAGGTTTGGTGTGGCGACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wu,K., Chung,L., Revill,W.P., Katz,L. and Reeves,C.D.
The FK520 gene cluster of Streptomyces hygroscopicus var.
ascomyceticus (ATC 14891) contains genes for biosynthesis of
unusual polyketide extender units
Gene 251 (1), 81-90 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptomyces hygroscopicus subsp. ascomyceticus
Streptomyces hygroscopicus subsp. ascomyceticus
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12667 GGCGGCCGTTGCGCGTTCGGCGCGCGACTTCATCGCGGCCGCCGCGGG 12715
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    856 AACGCGGGCCGGCACCTGCGGTGGATAACTTCCGGAAGTTCGTGGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptomycineae; Streptomycetaceae; Streptomyces.
1 (bases 1 to 77534)
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/variety="ascomyceticus"
/d_xref="taxon:132248"
complement(412. .1836)
/gene="fkbW"
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AF235504/c
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AASLAYGRKSVAWGCVGILRACRTAAVAHARTREQFGRPLGDHQLVAGHIADLWTAEQ
TAARVCEYSASHWDEGSPEWVPATILAKHVAAERAAGAATAAQVLASAGAREGHVVB
RAYRDAKLWEIIEGSEMCRYWLAQHALALPA"
complement (10988. .11248)
                                                                                                                                                                                                                                                                                                                                                        /protein id="AAF86389.1"
/db_xref="GI:9280391"
/translation="MTAPVKDDPVAHALVAFLKTKTRSDWPVDRDLFAEGGLTSLFAM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCTGCGAATCGACGACCTACGCAGCTTCATTTCAGTCGCTCAATCAGGCCACCTCACCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87 AACTGCCGAAAGATTAGGCATCCCGCAGCCCACATTTCCAGACGAATCAGCCGAGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5429 CÁCCGCGGÁÁCGGCTCAACATCTCCCÁGCCGACCCTGTCCÁGGGCCATCCGGCGGGCTGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               267 IGAAATCAAACGCCTCATGGACCCAGAAAAAGGCACAATCCGACTGGACTTCATGCATTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---- AGACGCCGCCGCGGGTGCGGACCGCGGAGCTGGCCGATGAGGCGTTCGTGGCACTGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4904 GCCGGTCTTCGGACTGCGCCAGATCACCGACCGGCTGTGCGCCGCCGCCGGCTGGATTCGTGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 77534;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELVVYLEKTFDVTIAGPDLQLANFRTVESMVALVHRLRAVDA" complement (11245. .12093)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
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                                                                                                                      VSITGTPETPSKVGLSIADICAGMYAVSGILTALLKRARTGRGSQLEVSMLEÄLGEWM
GYAEYYTRVGGTAPRAGASHATIAPYGPFTTRDGGTINLGLQNERBWASFCGVVLQR
PGLCDDPRFSGNADRVAHRTELDALVSEVTGTLTGEELVARLEEASIAYARQRTVREF
SEHPQLERGRWAPPDSPVGALEGLIPPVTFHGEHPRRLGRVPELGEHTESVLAMLAA
PHSADREEAGHAE"
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RYWEEAGVADRIDVRIGDARTVLTGLLDEAGAGPESFDMVFIDADKAGYPAYYEAALP
LVRRGGLIVVDNTLFFGRVADEAVQDPDTVAVRELNAALRDDDRVDLAMLTTADGVTL
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DOPRERAEVROPERTESORYTLLSLPERSPSPVGSTRRRLWYOGAFRADQA
REAVSGPDEDFLASLDLSWTTAPAGEBELSRYEELTLRTSQWATGVHYSDADLRACF
TDPAHEVLVVTWGDRFGFPHGAVGIILLEKKEPSTWHLKLLATSCRVVSFGAGATILNWL
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Search completed: April 13, 2005, 01:05:59 Job time : 4175 secs

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GenCore version 5.1.6

Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 12, 2005, 21:14:55; Search time 577 Seconds (without alignments)
9541.351 Million cell updates/sec
Title: US-09-826-909-1_COPY_232_1161
Sequence: 1 gtgaccatgggcaacgacggc......ggtatgcattagaagaggc 930
Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0
Searched: 4390206 seqs, 2959870667 residues
Total number of hits satisfying chosen parameters: 8780412
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aba91926 Corynebac	Aah68534 C glutami	Aah68193 C glutami	Aca01299 C. glutam	Aba91927 Corynebac	Aaa14651 Nucleotid	Abd13720 Pseudomon	Abd13492 Pseudomon	Abd13817 Pseudomon	Abd08478 Pseudomon	Abd08454 Pseudomon	Abd08440 Pseudomon	Aca43570 Prokaryot	Aah68525 C glutami	Aca26845 Prokaryot	Abd15300 Pseudomon	Abd04404 Pseudomon	Aca02128 C. glutam	Aah65438 C glutami	Abd04063 Pseudomon
SUMMARIES	ID	ABA91926	AAH68534	AAH68193	ACA01299	ABA91927	AAA14651	L ABD13720	L ABD13492	L ABD13817	L ABD08478	L ABD08454	L ABD08440	ACA43570	AAH68525	ACA26845	1 ABD15300	L ABD04404	ACA02128	AAH65438	L ABD04063
	Length DB	1364 6	309400 5	924 5	903 8	439 6	77536 3	927 1:	972 13	1482 13	987 1:	1485 13	1518 13	891 8	349980 5	954 8	1035 13	657 13	8808	882 5	1074 11
	% Query Match	100.0	100.0	99.4	97.1	47.2	14.1	7.3	7.3	7.3	9.9	9.9	9.9	6.5	6.5	6.4	6.4	6.2	6.2	6.2	6.2
	Score	930	930	924	903	439	131.2	68	68	68	61.4	61.4	61.4	9	9	59.8	59.5	57.8	57.8	57.8	57.8
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Novel lysR2 gene of coryneform bacteria encoding LysR2 protein which is transcription regulator, useful for fermentative production of L-lysine and L-valine and as a probe detecting polynucleotides encoding LysR2.

Claim 5; Page 36-38; 44pp; English.

Pfefferle W;

Kreutzer C,

Hermann T,

Moeckel B, Farwick M, WPI; 2002-227155/28. P-PSDB; AAM51006.

(DEGS ) DEGUSSA AG.

15-JUN-2001; 2001WO-EP0066808. 10-AUG-2000; 2000DE-01039047. 03-MAR-2001; 2001DE-01010346.

WO200212504-A1.

14-FEB-2002.

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DI.	15-MAY-2002		(fir	(first entry)	<u>3</u>		
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F				/product=	) ±`   [[		

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o;
The present sequence is that of the novel lysR2 gene of Corynebacterium glutamicum strain ATCC 13032. The gene codes for LysR2 protein (see AAM51006), a transcription regulator of the LysR family. The gene was identified in a cosmid gene library of ATCC 13032 using algorithms and sequence analysis programs. Vector pCR2.11ysR2int, which carries an internal fragment (see ABA91927) of the lysR2 gene, is claimed, and is deposited in Escherichia coli stain TOPIOF/pCR2.11ysR2int as DSM 13617. Also claimed are coryneform bacteria in which the lysR2 gene is attenuated, preferably eliminated, especially by deletion. These bacteria attenuated for the production of L-amino acids. Insertional mutagenesis of the lysR2 gene in the lysine producer C glutamicum BDM 5715 and the valine producer Brevibacterium lactofermentum FERM BP-1763 using vector pCR2.1lysRint in Emproved production of L-lysine and L-valine,
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                                                                                                                                                                                                                                                                                respectively. Further genes of L-amino acid biosynthetic pathways may also be manipulared. Polynucleotide sequences from the lysR2 gene may be used as hybridisation probes. e.g. in arrays, microarrays or DNA chips, for discovering related sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 930; DB 6; Length 1: Best Local Similarity 100.0%; Pred. No. 3.4e-264; Matches 930; Conservative 0; Mismatches 0; Indels
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sequences from the Corpnetors bacterium Corpnebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of corpnetors bacterium maeauring expression amount and analysing the expression profile or expression pattern of a gene derived from the expression profile or expression pattern of a gene derived from corpnetorm bacterium. Corpnetors are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office
                                                                                                                                                            1072 TTGGTGTGGCGACTCAACGCGGGGCCCGGCACCTGCGGTGGATAACTTCCGGAAGTTCGTG 1131
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                                                                                         1012 CTTCCCACAGTGGGAATCGTGCAACGCCCACTTAGTCCACCCGCTTATAGGGAACTAGGT
                                                                                                                             TTGGTGTGGCGACTCAACGCGGGCCCGGCACCTGCGGATAACTTCCGGAAGTTCGTG
                                                        CTTCCCACAGTGGGAATCGTGCAACGCCCACTTAGTCCACCCGCTTATAGGGAACTAGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid synthesis; vitamin; saccharide;
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Best Local Similarity 100.0%; Pred. No. 3.2e-263;
Matches 930; Conservative 0; Mismatches 0;
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Ikeda M, Ozaki A;
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03-AUG-2000; 2000JP-00280988
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Senoh A,
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Tateishi N,
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Ochiai K,

S, Hayashi M, Ozaki A;

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The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office
                                                                                                                                                                                                                                                                                                                                      Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analyzing
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            ourquerorm bacterium; amino acid synthesis; vitamin; saccharide; organic acid synthesis; ds.
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C glutamicum coding sequence fragment SEQ ID NO:
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Ikeda M,
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Tateishi 1
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                                                                        GTCGCTCAATCAGGCCACCTCACCGAAACTGCCGAAAGATTAGGCATCCCGCAGCCACCAC
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 GTGACCATGGGCAACGACGGCGGAGACCTGCGAATCGACGACCTACGCAGCTTCATTTCA
                                                       GTCGCTCAATCAGGCCACCTCACCGAAACTGCCGAAAGATTAGGCATCCCGCAGCCCACA
                                                                                                          CTTTCCAGACGAATCAGCCGAGTGGAAAACACGCAGGCACCCCACTTTCGACCGCGCC
                                                                                                                                   128303 CTTTCCAGACGAATCAGCCGAGTGGAAAAACACGCAGGCACCCCCACTTTTCGACGGCGC
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                                                                                                                                                                                                                                             128183 GTCGCAGAATTCAACTCCGCCGCAACTGAAATCAAACGCCTCATGGACCCAGAAAAAGGC
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                                   This invention describes a novel nucleic acid array involving Corynebacterium glutamicum polynucleotides. The arrays are used to analyse C. glutamicum, particularly for monitoring a fermentation process to determine expression levels of C. glutamicum cellular mRNA. Such monitoring particularly differentiates between expression levels of different strains of C. glutamicum and allows the adjustment of different culture and fermentation conditions. ACA00010-ACA02188 represent C. glutamicum derived polynucleotides described in the disclosure of the invention
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                                                                                                                                                                  TGCTCCTGGTAGATCGTGTTTTGGCTGATGAAACTGACCTCGCATTAGTTGGCCCCAAAC 475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FK-520; polyketide synthase; PKS; gene cluster; immunosuppressant; Streptomyces hygroscopicus var. ascomyceticus; immunophilin; FK-506 binding protein; polyketide compound; transplant rejection; graft-versus-host disease; uveltis; alopecia universalis; autoimmune chronic active hepatitis; inflammatory bowel disease; neutippe scleroderma; neutitipe scleroderma; neutite outgrowth; nerve regrowth; perve regrowth; parkinson's disease; Alzheimer's disease; traumatic spinal cord; brain injury;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleotide sequence of the FK-520 biosynthetic gene cluster.
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/*tag= a
/note= "fkbW gene"
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note= "fkbR2 gene"
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note= "fkbV gene"
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note= "fkbE gene"
808. .8052
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'note= "fkbG gene"
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156. .8824
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA14651 standard; DNA; 77536 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATGCATTAGCCGAAGAAGC 674
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is that of an internal fragment of the novel lysR2 gene of Corynebacterium glutamicum strain ATCC 13032. The gene fragment was obtained by PCR amplification of chromosomal DNA using the primers given in ABA91928 and ABA91929. It was used in the construction of claimed vector pCR2.1lysR2int, which is deposited in Bscherichia coli TOP10F as DSM 13617. The full-length LysR2 gene (see ABA91926) codes for LysR2 protein (see AMA91006), a transcription regulator of the LysR family. The invention provides coryneform bacteria in which the lysR2 gene is attenuated, preferably eliminated, especially by deletion. These bacteria are used in the production of L-amino acids. In an example of this, insertional mutageneshs of the lysR2 gene in the lysine producer C glutamicum DSM 5715 and in the valine producer Brevibacterium actorefermentum FERM BP-1763 using pCR2.1lysR2int improved yields of L-amino-dermentum FERM BP-1763 using pCR2.1lysR2int improved yields of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            236 CCATCGTCGCAGAATTCAACTCCGCCGCAACTGAAATCAAACGCCTCATGGACCCCAGAAA 295
    840
                                                                            841 GCACCTGCGGTGGATAACTTCCGGAAGTTCGTGGCGGGATCGAGTATGCATTAGAAGAG 900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel lysR2 gene of coryneform bacteria encoding LysR2 protein which is transcription regulator, useful for fermentative production of L-lysine and L-valine and as a probe detecting polynucleotides encoding LysR2.
    781 CCACTTAGTCCACCCGCTTATAGGGAACTAGGTTTGGTGTGGCGACTCAACGCGGGGCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LysR2; transcription; regulator; L-amino acid; L-valine; L-lysine; metabolic engineering; pCR2.1lysR2int; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 439;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 439 BP; 100 A; 135 C; 106 G; 98 T; 0 U; 0 Other;
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100.0%; Pred. No. 3.3e-119;
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Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                              ABA91927 standard; DNA; 439 BP.
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Matches 439; Conserv
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/*tag= n /note= "fkbH gene" complement(989410994) /*tag= i	/note= "fkb1 gene" complement(1098711247) /**:2- ;	/*tag= ] /note= "fkbJ gene" complement(1124412092)	/*tag= k /note= "fkbK gene" complement(1211313150)	/"tag= 1 /note= "fkbL gene" complement(13212, .23988)	//cdg= nl /note= "fkbC gene" complement(1345213662) /*tag= n	// cag= nacpe complement(1376114394)	//cay= "KR6" /note= "KR6" complement(1451715294)	/*tag= p /note= "BR6" complement(1543816587)	/*tag= q /note= "dehydratase domain (DH) 6" complement(1658717820)	/"tdg= r /note= "acyltransferase domain (AT) 6" complement(17820, .19053)	/*tag= s /note= "KS6" complement(1911619326)	/*tag= t /note= "ACP5" complement(1946420097)	/*tag= u /note= "KRS" complement(20241, .21420)	/*tag= V /note= "DH5" complement(2142022653)	/*tag= w /note= "AT5" complement(2265323892)	/*tag= x /note= "KS5" complement(2399246573)	= 9	/*tag= z /note= "ACP4" complement(24997, .26146)	/"tag= aa /note= "DH4 (inactive)" complement(2614627430) /*tag= ab	//cag- and //note= "AT4" (complement (27430, .28684)	/*tag= ac /note= "KS4" .complement(28750, .28960)	/"tag= ad /note= "ACP3" complement(2875028960)	/*tag= al /note= "DH2 (inactive)" complement(29092, .29740)
CDS	cns	CDS	cos	. sas	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	CDS	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc feature

/\*tag= ai /note= "ACP2" Complement (33823. .34480) /\*tag= aj /note= "KR2" complement (34606. .35749) /\*tag= ak complement (35749. .37144) /\*tag= am /note= "AT2" complement (37145. .38296) /\*tag= an /note= "KS2" complement(38371. .38581) complement (33505. .33715) \*tag= ah note= "KS3" misc\_feature CDS CDS CDS

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Matches 179; Conservative
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                                                                                                                                                                                                                          antibacterial
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                                                            29-JUL-2004
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ABD13720;
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Pred. No. 2.3e-09;
Pseudomonas aeruginosa polynucleotide #12324
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Local Similarity 49.2%;
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284 ACCTCACCGGCGAGGTCAGCGGCTGGTCCTGGCCACCACCACCACCACCACCTGC 343
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                                                  GGATGGTCCCCGAACTTATCCGAACATTCCGCGCCGAACACCCCAACGTAGAATTCCAAC 397
                                                                                Bacterial infection; gene; ds; Pseudomonas aeruginosa infection; antibacterial.
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                                  GCCTGCACCTGACCCGACCGGCGTGAGCGCATCGCCGCCCCTCGAACAGCACTCA
                                                                     Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;
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P-PSDB; ABO80246.
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27-JUL-1998;
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Gaps

; 0

Length 972;

7.3%; Score 68; DB 11; Length 972 49.2%; Pred. No. 2.3e-09; tive 0; Mismatches 185; Indels

Best Local Similarity 49.23 Matches 179; Conservative

Query Match

P-PSDB; ABO74907

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production of P. aeruginosa-derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas apecies using biochip technology. Sequences ABD1197-ABD17967 represent P. aeruginosa polynucleotides of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at
                                                                                                                                                                                                                                                                           99 ACAGCCTCAACACCTTCATCGCCATTGCCGAGACCGGCAGCTTCTCCGAAGCCGGCGAGC 158
                                                                                                                                                                                                                                                                                                          GATTAGGCATCCCGCAGCCCACCTTTCCAGACGAATCAGCCGAGTGGAAAAACACGCAG 157
                                                                                                                                                                                                                                                                                                                                        159 GCCTGCACCTGACCCAACCGGCGGTGAGCAAGCGCATCGCCGCCCTCGAACAGCAGCTCA 218
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                                                                                                                                              Sequence 1482 BP; 269 A; 555 C; 431 G; 227 T; 0 U; 0 Other;
                                                                                                                                                                          Score 68; DB 11; Length 14
Pred. No. 2.7e-09;
0; Mismatches 185; Indels
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The invention relates to Pseudomonas aeruginosa polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis and therapy, of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a prophylaxis and treatment of pathological conditions resulting from a correctial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using biochip technology. Sequences ABD01397-ABD17967 represent P. aeruginosa polynucleotides of the invention. Note: The sequence data for this patent did not form part of the printed specification but, was obtained in electronic format from USPTO at
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                                                          Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment opathological conditions resulting from bacterial infection.
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antibacterial.
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Pred. No. 2.1e-07;
0; Mismatches 196;
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                                                                                                                                                                                             Disclosure; SEQ ID NO 7082; 455pp; English
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Pred. No. 2.5e-07;
0; Mismatches 196; Indels
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Best Local Similarity 47.7%;
Matches 179; Conservative (
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Pseudomonas aeruginosa.
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The invention relates to Pseudomonas aeruginosa polypeptides and the polymucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, or the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant production of P. aeruginosa derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using biochip technology. Sequences ABD01397-of Pseudomonas species using biochip technology. Sequences ABD01397-of represent P. aeruginosa polymoutceotides of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at
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ilarity 47.7%; Pred. No. 2.5e-07;
Conservative 0; Mismatches 196;
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                                                                                                                                             crrcdecaccercredecrerecearcarceceacricareaeccaecacecer 1070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the 6113 antisense sequences given in the specification where expression of the mucleic acid inhibits proliferation of a cell. Also included are:
(1) a vector comprising a promoter operably linked to the mucleic acid encoding a polypeptide whose expression is inhibited by the autisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation; (8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
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                     207 AGGCCACGCCTTCCTCAACCACGCCAGCGCCATCGTCGCAGAATTCAACTCCGCCGCAAC
                                                                      267 TGAAATCAAACGCCTCATGGACCCAGAAAAAGGCACAATCCGACTGGACTTCATGCATTC
                                                                                            1189 GATTGİCGCCCTGCGCGAGAACGACCTGTGCGGCGAATTGCGCATCACCCCGATGAG
                                                                                                                      CTTGGGCACTTGGATGGTCCCCGAACTTATCCGAACATTCCGCGCGGAACACGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                            ds; prokaryotic essential gene; cell proliferation;
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Forsyth RA,
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Yamamoto R,
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                                                                                                                                                                                                                                                                                                                                    Prokaryotic essential gene #25227.
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06-SEP-2001; 2001US-00348993.
25-OCT-2001; 2001US-013-2023P.
08-FEB-2002; 2002US-00072851.
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Trawick JD,
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P-PSDB; ABU39700.
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identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids required for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids cauging the proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did alectoric form part of the printed specification, but was obtained in
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The invention relates to an isolated nucleic acid comprising any one of
the 6213 antisense sequences given in the specification where expression
of the nucleic acid inhibits proliferation of a cell. Also included are:
(1) a vector comprising a promoter operably linked to the nucleic acid
encoding a polypeptide whose expression is inhibited by the antisense
computed acid; (2) a host cell containing the vector; (3) an isolated
polypeptide or its fragment whose expression is inhibited by the
antisense nucleic acid; (4) an antibody capable of specifically binding
complypeptide; (5) producing the polypeptide; (6) inhibiting cellular
complification or the activity of a gene in an operon required for
proliferation, (7) identifying a compound that influences the activity of
compound for proliferation, or that inhibits cellular proliferation; (8)
compound a gene required for cellular proliferation or the biological
compound's activity, (11) a culture comprising strains in which the gene
compound's activity; (11) a culture comprising strains in which the cest
compound's activity; (11) a culture comprising strains in which the compound
corganism acts; (9) manufacturing an antibictic; (10) profiling a
compound's activity; (11) a culture comprising strains in which the extent
compound's activity; (11) a culture comprising strains in which the capanism. The antisense nucleic acids are useful for
conditieration of an organism. The antisense nucleic acids are useful for
dence of the contrained or condidence acids are useful for
conditieration or the isolate candidate molecules for rational
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for homologous nucleic acids required for cellular proliferation
isolate candidate molecules for rational drug discovery programs.
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Forsyth RA,
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6.4%; Score 59.8; DB 8;
3est Local Similarity 47.5%; Pred. No. 6.1e-07;
4atches 178; Conservative 0; Mismatches 197;
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Yamamoto R,
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Carr GJ,
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25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                     21-MAR-2002; 2002WO-US009107
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Trawick JD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        142308 AAGGCCGGAGAAATCCTCCACGAAGAAGCCCTCCGAACGCTTAGCAGGATGCAATCGGTA 142249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142488 GCACACATGCACCTCAATCAGCTCGAATTTTTCATCGCAGTAGCCCAACACGGACAGATC 142429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     142428 AACCGCGCCGCCGAGAACTCCTCATTTCCCAACCCGCTCTCAGCCGACAGATCTCCGCA 142369
                                                                                                                                                                                                                                                                                                                                                                                               The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria and organic actived from acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGAGACCTGCGAATCGACGACCTACGCAGCTTCATTCAGTCGCTCAATCAGGCCACCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82 ACCGAAACTGCCGAAAGATTAGGCATCCCGCAGCCCACACTTTCCAGACGAATCAGCCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 349980 BP; 80289 A; 91081 C; 97378 G; 81232 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                     Yokoi H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ds; prokaryotic essential gene; cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 6.5%; Score 60; DB 5; Length 349980; Best Local Similarity 51.5%; Pred. No. 6.2e-06; Matches 138; Conservative 0; Mismatches 130; Indels 0;
                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 7060; 246pp + Sequence Listing; English.
                                                                                                                                                                     Ochiai K,
                                                                                                                                                                S, Hayashi M,
Ozaki A;
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Ikeda M,
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                                       99JP-00377484.
2000JP-00159162.
2000JP-00280988.
18-DEC-2000; 2000EP-00127688.
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Senoh A,
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03-AUG-2000;
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Tateishi N,
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Zyskind JW; Xu HH;

145 GAAAAACACGCAGGCACCCCACTTTTCGACCGCCGGCCGCAAACTCGTCCTCAACCAA 204

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Run on:

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/db xref="taxon:7159"
/clone="NotreDame Liverpool-105A23"
/clone=lb="Notre Dame Liverpool"
/note="Vector: pECBAC1; Site_1: Hind III; The library was prepared from whole body tissue of newly hatched L1 larvae by David Severson at the University of Notre Dame and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCTCACCGAAACTGCCGAAAGATTAGGCATCCCGCAGCCCACACTTTCCAGACGAATCAG 137
                                      pacs1-60
pacs2-164
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Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes;
                                                                                                                              UMC-Dend
                                                                                                                                                                                                                                                                                                                                                                       CC842306 105A23.T7 Notre Dame Liverpool Aedes aegypti genomic clone NotreDame Liverpool 960001.105A23, genomic survey sequence.
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                                     BZ551243
AY08024
AX08034
BZ548324
BZ578976
BZ578976
BZ57865
BZ578104
BH190115
AL066784
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AL065923
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stegomyia.

1 (bases 1 to 760)

Loftus, B., Shetty, J., Knudson, D. and Severson, D.
BAC end sequencing of Aedes aegypti
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: enta@tigr.org
Library was provided by David Severson
Sed primer: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aedes aegypti (yellow fever mosquito)
Aedes aegypti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1. 760
/organism="Aedes aegypti"
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                                                                                                                                                                                                                                                                                                         ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Department of Eukaryotic Genomics
                                   BZ551243
AY080924
AY080934
BZ548324
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CNS0073W
CL982230
CNS006U
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CNS006U
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Contact: Brendan Loftus
                                                                                                                                                                                                                                                                                                                                                                                                                            CC842306.1 GI:33188999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         by David sever.
Hongbin Zhang"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 301-838-3543
Fax: 301-838-0208
Seg primer: T7
Class: BAC ends.
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BZ443106 1459405.9
BZ566287 pacs2-164
AZ933780 BJ_BA000
BZ579898 msh2 832.
BZ422864 1459405.b
CF933278 TrEST-B03
BZ556936 pacs1-60
                                                                                     April 12, 2005, 23:13:05; Search time 3101 Seconds (without alignments) 11415.598 Million cell updates/sec
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Compugen Ltd.
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930
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Copyright (c) 1993 - 2005
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Listing first 45 summaries
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87 AACTGCCGAAAGATTAGGCATCCCGCAGCCCACACTTCCAGACGAATCAGCCGAGTGGA
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                                                                                                                                                                                                                                                                                                                           86
                    62
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Pseudomonas aeruginosa
Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales;
Pseudomonadacae; Pseudomonas.

(Dassel 1 co 766)
Spencer, D. H., Raymond, C. K., Smith, E. E., Sims, E. E., Hastings, M.,
Burns, J. L., Kaul, R. and Olsen, M. V.
Whole-Genome-Sequence variation among multiple isolates of
Psedomonas aeruginosa library
J. Bacteriol. (2002) In press
CTTCACCCGCGCGGAAAAACTGTTCGTCACCCACCCACCACCACCACCAGATGCTGCG
                                                  63 GCATCTGGAAGAGGAGCTGGAATGCACGCTGCTGATCCGCGAAGGCCGCAAGCTGCGCCT
                                                                                                            CAACCAACGACGCCTTCCTCAACCACGCCAGCGCCATCGTCGCAGAATTCAACTC
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genomic survey sequence.
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/do_clone="msh2 307"
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/note="Tenvironmental isolate. Whole genomic shotgun
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Larity 52.7%; Pred. No. 3.4e-05;
Conservative 0; Mismatches 112; Indels
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University of Washington
Box 352145, Seattle, WA 98105-2145,
Tel: 2062216954
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/mol_type="genomic DNA"
/strain="MSH"
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Whole-Genome-Sequence variation among multiple isolates of Psedomonas acruginosa library
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Contact: Chris K. Raymond
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Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
Fax: 2066857244
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Class: shotgun.
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Whole-Genome-Sequence variation among multiple isolates of
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/strain="2-164"
/db_xref="taxon:287"
/clone="pacs2-164" 766"
/clone lib="pacs2-164"
/note="clinical isolate 2-164 Whole genomic shotgun
                    Whole-Genome-Sequence variation among multiple isolates Psedomonas aeruginosa library J. Bacteriol. (2002) In press Contact: Chris K. Raymond
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                                                                                                      Genome Center
University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
Fax: 2066857244
Email: craymond@u.washington.edu
Class: shotgun.
Burns, J.L., Kaul, R. and Olsen, M.V.
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Pseudomonadaceae, Pseudomonas.
1 (bases 1 to 1350)
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Whole-Genome-Sequence variation among multiple isolates of Psedomonas aeruginosa library
J. Bacteriol. (2002) In press
Contact: Chris K. Raymond
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1 (Dases 1 to 1175)
Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M.,
                  1350 bp DNA linear GSS 17-DEC.
pacs1-60_4884.x1 pacs1-60 Pseudomonas aeruginosa genomic clone
pacs1-60_4884, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Fax: 2066857244
Email: craymond@u.washington.edu
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Location/Qualifiers
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Whole-Genome-Sequence variation among multiple isolates of Psedomonas acruginosa library
J. Bacteriol. (2002) In press
Contact: Chris K. Raymond
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Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales,
Pseudomonadacae; Pseudomonas.
1 (bases 1 to 1077)
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/mol_type="genomic DNA"

/strain="WAH"

/db xref="taxon:287"

/clone="msh2_3292"

/clone_lb="msh"

/clone_lb="msh"

/lone_lb="msh"
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/organism="Pseudomonas aeruginosa"
                                               Genome Center
University of Washington
Box 352145, Seattle, WA 98105-2145,
TT-1: 2062216954
Fax: 2066857244
Email: craymond@u.washington.edu
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University of Washington
Box 352145, Seattle, WA 98105-2145,
Tel: 2062216954
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Psedomonas aeruginosa library
J. Bacteriol. (2002) In press
Contact: Chris K. Raymond
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/db_xref="taxon:287"
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/clone_lib="pac82-164"
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library."
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Pred. No. 7e-05;
0; Mismatches 223; Indels
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/db_xref="taxon:9940"
/clone="Oa_splbn_10N24"
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Seg primer: Mlareverse
High quality sequence start: 6
High quality sequence stop: 550.
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Veterinary Blomedical Sciences
University of Edinburgh
Summerhall Square, Edinburgh, E
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Best Local Similarity 46.0°
Matches 190; Conservative
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CO202977
Oa_splbn_14E11_M13_Reverse Sheep spleen\brain pSport1 library Ovis aries cDNA clone Oa_splbn_14E11_5', mRNA sequence.
                                                                                                186 CCGCCGAGCAGTTGGGCATCGCCCCCACCGACCTGGAGACCAGGACATGGAAA 445
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Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Caprinae; Ovis.
                                                                  CTGCCGAAAGATTAGGCATCCCGCAGCCCACACTTTCCAGACGAATCAGCCGAGTGGAAA
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/clone lib="Sheep spleen\brain pSport1 library"
/note="Vector: pSport1"
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Gossner, A. and Hopkins, J.
Gossner, A. and Hopkins, J.
Ovine splem\\text{Learn cDNA} library
Unpublished (2004)
Contact: J Hopkins
Veterinary Biomedical Sciences
University of Edinburgh
Summerhall Square, Edinburgh, EH9 10H.
Email: j.hopkins@ed.ac.uk
Plate: 14 row: E column: 11
Seq primer: M13 Reverse
High quality sequence start: 6
High quality sequence start: 6
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/mol_type="mRNA"
/db_xref="taxon:9940"
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1 (bases 1 to 768)

Gossner, A. and Hopkins, J.
Ovine spleen\brain cDNA library
Unpublished (2004)
Contact: J Hopkins
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/clone lib="Sheep spleen\brain pSport1 library"
/note="Vector: pSport1"
/clone_lib="Sheep spleen\brain pSport1 library"
/note="Vector: pSport1"
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Best Local Similarity 48.9%; Pred. No. 9.6e-05;
Matches 151; Conservative 0; Mismatches 158;
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High quality sequence stop: 548.
Location/Qualifiers
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/organism="Ovis aries"
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University of Edinburgh
Summerhall Square, Edinburgh, E
Email: j.hopkins@ed.ac.uk
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/clone="pacs2-164_6003"
/clone_lib="pacs2-164"
/note="clinical isolate 2-164 Whole genomic shotgun
library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hasti. Burns, J.L., Kaul, R. and Olsen, M.V.
Whole-Genome-Sequence variation among multiple isolates bedomonas aeruginosa library
J. Bacteriol. (2002) In press
Contact: Chris K. Raymond
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Pred. No. 0.00015;
0; Mismatches 154; Indels
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University of Washington
Box 321145, Seattle, WA 98105-2145,
Tel: 206216954
Fax: 2066857244
Email: craymond@u.washington.edu
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/strain="2-164"
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Pseudomonadaceae, Pseudomonas.
1 (bases 1 to 817)
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/note="Site_1: Xba I; Site_2: Xba I; The vector was
digested with XbaI is Site_2: Xba I; The vector was
digested with XbaI and one nucleotide was added by fill in
the recessive 3' end. The genomic DNA was nebulized,
end repaired, adaptor ligated and size fractionated using
sephadex. The resulting fragments were between 0.8 and 3
kb and were cloned into the vector (:x/y reads in M13mp19,
b)g reads in pUC19). The same ligation was transformed
into DHSa."
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/mol_type="genomic DNA"
/db_xref="taxon:4558"
/clone="id59405"
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Location/Qualifiers
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Plate: id59 row: d column: 05
Seq primer: -21M13UnivRev
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Sorghum bicolor
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msh2 832.y2 msh Pseudomonas aeruginosa genomic clone msh2_832,
genomic survey sequence.
BZ57998
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                                                                                                                                                                                   Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadacee; Pseudomonas.

1 (Dasea I to 1072)

S Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M., Burns, J.L., Kaul, R. and Olsen, M.V.
Whole-Genome-Sequence variation among multiple isolates of Psedomonas acruginosa library

J. Bacteriol. (2002) In press
Contact: Chris K. Raymond
Genome Center
University of Washington
Box 352145, Seattle, WA 98105-2145, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sorghum bicolor (sorghum)
Sorghum bicolor
Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 451)
Rabinowicz, P.D., O'Shaughnessy, A.L., Balija, V., Dedhia, N.,
Katzenburger, F., King, L., Miller, B., Muller, S., Nascimento, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           272 Acadecreaacacerrearesecarrecesaacesecaerrerecesaseceseceses
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         332 GCCTGCACCTGACCCAACCGGCGGTGAGCAAGCGCATCGCCGTCCTCGAACAGCAGCTCA 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        392 ATGCCCGGCTGTTCGACCGGGTCGGCCGCGAGGTCAACCTCACCGAGGCCCGGCGCGCCC 451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:287"
/clone="man2 832"
/clone lib="man2 812"
/note="Environmental isolate. Whole genomic shotgun
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52.4%; Pred. No. 0.00023;
ive 0; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Pseudomonas aeruginosa"
/mol_type="genomic DNA"
/strain="MSH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fax: 2066857244
Email: craymond@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                 BZ579898.1 GI:27214959
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BZ422864.1 GI:26371550
                                                                                                                                            Pseudomonas aeruginosa
                                                                                                                                                                  Pseudomonas aeruginosa
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Matches 121; Conservative
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                                                                                                                                                                                   AZ933780 674 bp DNA linear GSS 24-APR-2001 BJ Ba0001E08r B. japonicum BAC library Bradyrhizobium japonicum genomic, genomic survey sequence. AZ933780 GI:13775840
                                                                                                                                                                                                                                                                                                                       Bradyrhizobium japonicum
Bradyrhizobium japonicum
Bradyrhizobium japonicum
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
1 (baees 1 to 674)
Tomkins,J.P., Wood,T.C., Stacey,M.G., Loh,J.T., Judd,A.,
Goicoechea,J.L., Stacey,G., Sadowsky,M.J. and Wing,R.A.
A marker-dense, sequence-ready map of the Bradyrhizobium japonicum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             334 Agéricadeacerricagrirecerecedegegerecedeacerecenedesecerecedeses 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 TAGGCATCCCGCAGCCCACACTTTCCAGACGAATCAGCCGAGTGGAAAAACACGCAGGCA 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCAACCACGCCAGCGCCATCGTCGCAGAATTCAACTCCGCCGCAACTGAAATCAAACGCC 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tch 5.9%; Score 55.2; DB 8; Length 674; al Similarity 49.1%; Pred. No. 0.00018; 144; Conservative 0; Mismatches 149; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:375"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Organism="Bradyrhizobium japonicum"
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|strain="USDA110"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Fmail: rwing@clemson.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome Res. 11 (8), 1434-1440 (2001)
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Location/Qualifiers
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                                                                    422 ACTTCCAGCTCCAGGAAG 439
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RESULT 14 BZ579898

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Zutavern,T., Palmer,L., McCombie,W.R. and Martienssen,R.A.
Genomic shotgun sequences from Sorghum bicolor (methyl-filtered)
Lupublished (2002)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Hazen Genome Sequencing Center
Cold Spring Hazen Genome Sequencing Center
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8874
Fax: 516 367 8874
Email: mccombie@ceshl.org
Plate: id59 row: d column: 05
Seq primer: -21M13UnivFwd
Class: shotgun
High quality sequence stop: 451.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_nost="bfsa" (Cone liba-wGS-SbicolorF (DH5a methyl filtered)" (Cone liba-wGS-SbicolorF (DH5a methyl filtered)" (Cone liba-wGS-SbicolorF (DH5a i, The vector was digested with Xbai and one nucleotide was added by fill in the recessive 3' end. The genomic DNA was nebulized, end repaired, adaptor ligated and size fractionated using sephadex. The resulting fragments were between 0.8 and 3 kb and were cloned into the vector (.x/y reads in M13mp19, .b/g reads in pUC19). The same ligation was transformed into DH5a."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85 GAAACTGCCGAAAGATTAGGCATCCCGCAGCCCACATTTCCAGACGAATCAGCCGAGTG 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 GATATGGAACTTCGCCACCTGCGTTATTTCGTTGCCGTTGCTGAAACGCAGCACTTTACC 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25 GACCTGCGAATCGACGTACGCAGCTTCATTTCAGTCGCTCAATCAGGCCACCTCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   205 CGAGGCCACGCCTTCCTCAACCACGCCAGCGCCATCGT 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Sorghum bicolor" '
/mol_type="genomic DNA" |
/db_xref="taxon:4558" |
/clone="id59405"
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Sequence 3308, Ap
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3414, Ap
3336, Ap
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Sequence 1, Appli
                                                                                     April 12, 2005, 23:32:55 ; Search time 206 Seconds (without alignments) 7387.075 Million cell updates/sec
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(cgn2_6/ptodata/1/ina/5B_COMB.seq:*

(cgn2_6/ptodata/1/ina/6A_COMB.seq:*

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(cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
            GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-940-316B-1

US-09-252-991A-12324

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US-09-252-991A-7058

US-09-252-991A-7064

US-09-252-991A-7044

US-09-252-991A-3008

US-09-252-991A-3008

US-09-252-991A-3414

US-09-252-991A-5279

US-09-252-991A-5279

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US-09-252-991A-3414

US-09-252-991A-3168

US-09-252-991A-3208

US-09-252-991A-3208

US-09-252-991A-3208

US-09-252-991A-3208

US-09-252-991A-3414

US-09-252-991A-12330

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                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                              1202784 segs, 818138359 residues
                                                                                                                                                US-09-826-909-1_COPY_232_1161
930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                                                                                                          Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                 nucleic search, using sw model
                                                                                                                                                                                                     IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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seq length: 2000000000
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Match Length
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1485
1518
1035
657
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129.6
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54.8
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61.4
61.4
                                                                                                                                                              Perfect score:
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Maximum DB
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                                                                                                                                                                                                                                              Searched:
                                                                                                                                                                                                                                                                                                                                                                                                  Database
                                                                                           Run on:
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No.
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3462,

Sequence

US-09-252-991A-3486 US-09-252-991A-3438 US-09-252-991A-3462

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5430
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                                                                                                                                  6167, 7
12061,
                                                                                       6298, 1
11951,
1429, 1
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1463,
1511,
1663,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87 AACTIGCCGAAAGATTAGGCATCCCGCAGCCCACACTTTCCAGACGAATCAGCCGAGTGGA
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APPLICANT: REEVES, CHRISTOPHER
APPLICANT: REEVES, CHRISTOPHER
APPLICANT: CHU, DANIEL
APPLICANT: SANTI, DANIEL
TITLE OF INVENTION: CONSTRUCTS THEREFOR
TITLE OF INVENTION: UNBER: US 60/139,650
PRIOR APPLICATION NUMBER: US 60/139,650
PRIOR PILING DATE: 1999-03-11
PRIOR FILING DATE: 1999-03-11
PRIOR FILING DATE: 1999-03-11
PRIOR FILING DATE: 1999-03-11
SPRIOR FILING DATE: 1999-03-11
PRIOR FILING DATE: 1999-03-11
SPRIOR FILING DATE: 1999-10-02
NUMBER OF SEQ ID NOS: 72
SUSTIMARE: FREESEQ FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA
                                                                          Sequence                                                                                                                                                                                                                        Sequence 1
Sequence 1
Sequence 6
                  Sequence
Sequence
Sequence
                                                            Sequence
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US-09-902-540-8724

US-09-902-540-3768

US-09-902-540-1182

US-09-902-540-1183

US-09-902-540-1183

US-09-902-540-1183

US-09-252-991A-6129

US-09-252-991A-6167

US-09-252-991A-6167

US-09-252-991A-6167

US-09-252-991A-12061

US-09-252-991A-12061

US-09-252-991A-1511

US-09-252-991A-1511

US-09-252-991A-1511

US-09-252-991A-1511

US-09-252-991A-1511

US-09-252-991A-1511

US-09-252-991A-1511

US-09-252-991A-12230

US-09-252-991A-12230
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Pred. No. 4.3e-28;
0; Mismatches 349;
                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Streptomyces hygroscopicus
                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09410551B
Patent No. 6503737
GENERAL INFORMATION:
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50.7%;
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   Similarity
    RESULT 1
US-09-410-551B-1/c
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LOCATION: (52)
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Best Local
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Sequence 13324, Application US/09252991A

Patent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION UNMERR: US/09/252, 991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR PRILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR PLING DATE: US 60/094,190
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                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                           Length 77536;
                                                                                                                                                                                                                                                        Indels
                                                                                                                                           DB 4;
                                                                                                                                                                                                                                                        Mismatches 349;
                                                                                                                                     Score 129.6; DB 4
Pred. No. 4.3e-28;
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50.7%;
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US-09-252-991A-12324
                        US-09-940-316B-1
                                                                                                                                                                                                                                                        Matches 374;
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APPLICANT: CHU, DANIEL
APPLICANT: KHOSLA, CHAITAN
APPLICANT: KHOSLA, CHAITAN
APPLICANT: SANTI, DANIEL
APPLICANT: SANTI, DANIEL
APPLICANT: WU, KAI
TITLE OF INVENTION: GENE CLUSTER
TITLE REFERENCE: 30062-20026.11
CURRENT APPLICATION NUMBER: US 60/139,650
PRIOR APPLICATION NUMBER: US 60/139,650
PRIOR FILING DATE: 1999-10-01
PRIOR FILING DATE: 1999-03-11
PRIOR FILING DATE: 1999-03-11
PRIOR FILING DATE: 1999-03-11
PRIOR FILING DATE: 1999-03-11
SPRIOR FILING DATE: 1999-03-11
SPRIOR FILING DATE: 1999-03-11
SPRIOR SEQ ID NOS: 72
SOFTWARE: FRASERQ FOR Windows Version 4.0
SEQ ID NO 1
LEMCTH: 7536
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Sequence 1, Application US/09940316B
Patent No. 6759536
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APPLICANT: KOSAN BIOSCIENCES
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NAME/KEY: CDS
LOCATION: (52275)...(71465)
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Sequence 12421, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
                   830 GCCTGCACCTGACCCAACCGGCGGTGAGCGAAGCGCATCGCCGCCCTCGAACAGCAGCTCA 771
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Patent No. 6551795

GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERGIGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-18
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PRIOR FILING DATE: 1998-07-2
NUMBER OF SEQ ID NOS: 33142
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LENGTH: 927
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Best Local Similarity 49.24
Matches 179, Conservative
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Best Local Similarity 49.2
Matches 179; Conservative
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APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AEROGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AEROGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AEROGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 7044
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Pred. No. 3e-08;
0; Mismatches 196;
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47.7%; Pred. No. 3.1e-08;
iive 0; Mismatches 196;
    US 60/094,190
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US-09-252-991A-7044/c
S. Sequence 7044, Application US/09252991A
; Patent No. 6551795
                                                                                                                                                                                                                                        ORGANISM: Pseudomonas aeruginosa US-09-252-991A-7058
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                                 1998-07-27
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Matches 179; Conservative
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Best Local Similarity 47.7
Matches 179; Conservative
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1998-0
NUMBER OF SEQ ID NOS: 331
SEQ ID NO 7058
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US-09-252-991A-7044
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                                                                                                                                                                                                                                                        Patent No. 6551795
GENERAL INFORMATION:
APPLICANT:
MATC J. Rubenfield et al.
TITLE OF INVENTION: WUCLEIC ACID AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
PRIOR PILING DATE: 1998-07-27
PRIOR PILING DATE: 1998-07-27
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Patent No. 6551795
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
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Pred. No. 2.5e-08;
0; Mismatches 196;
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Best Local Similarity 47.7%;
Matches 179; Conservative
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SEQ ID NO 7082
TCCA 401
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Sequence 2667. We set the control of                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196_136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-27
PRIOR FILING DATE: 1998-07-27
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Pred. No. 2.5e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3008, Application US/09252991A
Patent No. 6551795
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US 609/252,991A

CURRENT PILING DATE: 1999-02-18

PRIOR PILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 13964
1249 CGGGCATTTCTTCTACAAGGCCGCCAAGGCCTCGCTGCAGGAACTCAACAACGCCGCGGA 1190
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    TITLE OF INVENTION:
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PLING DATE: 1998-02-18
PRIOR PLING DATE: 1998-02-18
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                                                                                                                                                                          Indels
                                                                            Query Match 6.2%; Score 57.8; DB 4; 1
Best Local Similarity 52.7%; Pred. No. 3.2e-07;
Matches 125; Conservative 0; Mismatches 112;
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Pred. No. 2.8e-07;
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APPLICANT: Marc J. Rubenfield et al.
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ORGANISM: Pseudomonas aeruginosa
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Matches 121; Conservative
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US-09-252-991A-5279
US-09-252-991A-2667
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS:
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
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PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
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FRIOR APPLICATION NUMBER: US 60/094,190
FRIOR PILING DATE: 1998-07-27
SEQ ID NO 5279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Pseudomonas aeruginosa
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GENERAL INFORMATION:
APPLICANT:
APPLICANT:
MACC J. RUBERIEL ALID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS.
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 5260
LENGTH: 2592
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                                         215 CCTTCCTCAACCACGCCAAGCGCCATCGTCGCAGAATTCAACTCCGCC 261
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                                                                                                                             RESULT 15
8.09-252-991A-5260/c
; Sequence 5260, Application US/09252991A
; Patent No. 6551795
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US-09-826-909-1

| Sequence 1, Application US/09926909 |
| Patent No. US20020081674A1 |
| Patent No. US20020081674A1 |
| GENERAL INFORMATION: |
| APPLICANT: PARMICK, MIKE |
| APPLICANT: FARMICK, MALER |
| APPLICANT: REDOTED |
| APPLICANT: REDOTED |
| APPLICANT: RECOTED |
| APPLICANT: RESERVE: 2005100 |
| FILE REFERENCE: 205551USOX |
| CURRENT APPLICATION NUMBER: US/09/826,909 |
| CURRENT FILING DATE: 2000-08-10 |
| PRIOR FILING DATE: 2000-08-10 |
| PRIOR FILING DATE: 2000-08-10 |
| PRIOR FILING DATE: 2001-03-03 |
| NUMBER OF SEQ ID NOS: 5 |
| SOFTHARE: PatentIn version 3:1
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15 US-10-156-761-4980
15 US-10-156-761-3218
15 US-10-156-761-3218
17 US-10-282-122A-31440
17 US-10-282-122A-14715
18 US-10-156-761-2141
9 US-09-938-641-1
19 US-09-938-641-1
19 US-10-485-710-1
19 US-10-485-710-1
19 US-10-398-221-244
17 US-10-398-221-2058
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Best Local Similarity 100.
Matches 930; Conservative
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; LOCATION: (232)..(1161)
; OTHER INFORMATION:
US-09-826-909-1
      SEQ ID NO 1
LENGTH: 1364
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Sequence 3228, Ap
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Listing first 45 summaries
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                                                                                                                           GTGGCTCAATCAGGCCACCTCACCGAAACTGCCGGAAAGATTAGGCATCCGGAGCCCACA
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Sequence 1, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO

RESULT 2 US-09-738-626-1/c

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601 GCGGAAGAACCTTTCGTGGCGATGCGAGCTTTCGGCACCCGACTCCTCATGGATGCA 660 ...
3127823 GCGGAAGAACCTTTCGTGGCGATGCGAGGTTTCGGCACCCCGACTCCTCATGGATGCA 3127764
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100.0%; Score 930; DB 9; L
Best Local Similarity 100.0%; Pred. No. 1.7e-291;
Matches 930; Conservative 0; Mismatches 0;
                                        APPLICANT: TATEISHI, NACKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: KEBA, MAGATO
APPLICANT: KEBA, MAGATO
TITLE OF INVENTION: NOVEL POLYNUCLECTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT APPLICATION NUMBER: UP 99/377484
PRIOR PILING DATE: 2000-12-18
PRIOR FILING DATE: 2000-04-07
SOFTWARE: PATENTION NUMBER: UP 00/159162
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENTIN VET: 3.0
SEQ ID NO. 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA; ORGANISM: Corynebacterium glutamicum US-09-738-626-1
OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
OZAKI, AKIO
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APPLICANT: MOECKEL, BETTINA
APPLICANT: MOECKEL, BETTINA
APPLICANT: FARMICK, MIKE
APPLICANT: FRAMICK, MIKE
APPLICANT: KREUTZER, CAROLINE
APPLICANT: FFFFERLE, WALTER
TITLE OF INVENTION: NUCLECTIOE SEQUENCES FOR ENCODING OF THE LYSR2-GENE
TITLE OF INVENTION: NUCLECTION SEQUENCES
CURRENT FILING DATE: 2002-05-01
PRIOR APPLICATION NUMBER: DE 100 39 047.1
PRIOR APPLICATION NUMBER: DE 100 346.8
PRIOR PILING DATE: 2001-03-03
PRIOR FILING DATE: 2001-03-03
PRIOR FILING DATE: 2001-03-03
SOFTWARE: PALENTIN VERSION 3.1
SEQ ID NOS: 5
SOFTWARE: PALENTIN VERSION 3.1
SEQ ID NOS: 5
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SEQ ID NOS: 5
SEQ ID NOS: 5
TYPE: DNA
                                                                                                                                                                                                                                                      841 TGGCGACTCAACGCGGGGCCGGCACCTGCGGTGGATAACTTCCGGAAGTTCGTGGCGGGA 900
                                                                                                                                                                                               GAAGAAGCCGGTTTTGTTCCCAATGTGGTTTTCGAATCCATGGAACTCACCACCGTCGCA 726
                                            241 GAATTCAACTCCGCCGCAACTGAAATCAAAGCCTCATGGACCCAGAAAAAGGCACAAATC
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                         3127763 TTAGCCGAAGAAGCCGGTTTTGTTCCCAATGTGGGTTTTCGAATCCATGGAACCCACC
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Best Local Similarity 100.0%; Pred. No. 7.8e-291;
Matches 924; Conservative 0; Mismatches 0; Indels
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PUDICANT: NAKAGAMA, SATOSHI

APPLICANT: NAKAGAMA, SATOSHI

APPLICANT: ANDO SEIKO

APPLICANT: HAYASHI, MIKIRO

APPLICANT: HAYASHI, MIKIRO

APPLICANT: TATELSHI, NACKO

APPLICANT: YOKOI, HARUHIKO

APPLICANT: YOKOI, HARUHIKO

APPLICANT: YOKOI, HARUHIKO

APPLICANT: SENOH, AKTHIRO

APPLICANT: SENOH, AKTHIRO

APPLICANT: SENOH, MASATO

APPLICANT: SENOH, MASATO

APPLICANT: SENOH, MASATO

APPLICANT: OZAKI, AKIO

TITLE OF INVENTION: NOVEL FOLYNUCLEOTIDES

FILE REFRERENE: 29-125

CURRENT FILING DATE: 2000-12-18

PRIOR PILING DATE: 1999-12-16

PRIOR PELING DATE: 1999-12-16

PRIOR PILING DATE: 1999-12-16

PRIOR PILING DATE: 2000-04-07

PRIOR PILING DATE: 2000-08-03

NUMBER OF SEQ ID NOS: 7059

SOFTWARE: PRECENTIN VET: 3.0

SOFTWARE: PRECENTIN VET: 3.0
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3228, Application US/09738626
Publication No. US20020197605A1
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US-09-738-626-3228
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661
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5369 GCGACGAGTGGGCGTGCCGCTGTTCGACCGGCACCAGAACCGGCTCCGGCTCAACAAGTA 5310
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                                                                                                                                                                                                                                                                                                                                                                                     AGGCCACGCCTTCCTCAACCACGCCAGCGCCATCGTCGCAGAATTCAACTCCGCCGCAAC
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                                                                                                                                                                        AACTGCCGAAAGATTAGGCATCCCGCAGCCCACACTTCCAGACGAATCAGCCGAGTGGA
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                                                                                                                                27 CCTGCGAATCGACGACCTACGCAGCTTCATTTCAGTCGCTCAATCAGGCCACCTCACCGA
                                                                                                                                                                                                                                                      267 TGAAATCAAACGCCTCATGGACCCAGAAAAGGCACAATCCGACTGGACTTCATGCATTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              687 CAATGIGGTTTTCGAATCCATGGAACTCACCACCGTCGCAGGGCTTGTCAGCGCAGGTCT
                                                DB 10; Length 77536;
                                                                                         15;
                                                                                       0; Mismatches 349;
                                             Score 129.6; DB 1
Pred. No. 1.1e-30;
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAMA, JUN
APPLICANT: HORIKAWA, JUN
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
ITILE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
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US-10-156-761-3347
Sequence 3347, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
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                                             13.9%;
50.7%;
                                                                                       Matches 374; Conservative
                                                                 Similarity
      US-09-940-316B-1
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US-90-940-116B-1/C
Sequence 1, Application US/09940316B
Publication No. US20030175901A1
GENERAL INFORMATION:
GENERAL INFORMATION:
HERVER, INFORMATION:
APPLICANT: REEVES, CHRISTOPHER
APPLICANT: CHU, DANIEL
APPLICANT: CHU, DANIEL
APPLICANT: GENERALE, CHAITAN
APPLICANT: WIGHTON TAIL
TITLE OF INVENTION: GENE CLUSTER
TITLE OF INVENTION: GENE CLUSTER
TITLE OF INVENTION GENE CLUSTER
FILE REPREBRENCE: 30062-50026-11
CURRENT APPLICATION NUMBER: 09/410,551
FRIOR PELING DATE: 1999-10-01
PRIOR PELING DATE: 1999-06-17
PRIOR APPLICATION NUMBER: US 60/123,810
PRIOR PELING DATE: 1999-06-17
PRIOR APPLICATION NUMBER: US 60/123,810
PRIOR PELING DATE: 1999-03-11
PRIOR PELING DATE: 1998-10-02
NUMBER OF SEQ ID NOS: 72
NUMBER OF SEQ ID NOS: 72
SEQ ID NO 1
SERVING DATE: NUMBER: US 60/102,748
SEQ ID NO 1
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                                                                                                                                                                                                                                   296 AAGGCACAATCCGACTGGACTTCATGCATTCCTTGGGCACTTGGATGGTCCCCGAACTTA
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                                                                 Length 439;
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                                                                                                        Indels
                                                                 DB 9; Le
1.5e-132;
                                                47.2%; Scc...
100.0%; Pred. No. 1...
0; Mismatches
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ORGANISM: Streptomyces hygroscopicus
FEATURE:
NAME/KEY: CDS
LOCATION: (52275)...(71465)
; ORGANISM: Corynebacterium glutamicum
US-09-826-909-3
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                                                           Query Match
Best Local Similarity 100.
Matches 439; Conservative
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Pred. No. 1.2e-23;
0; Mismatches 421; Indels 18; Ga
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: ISHIKAWA, JUN
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SAKKKI, YOSHIVUKI
APPLICANT: HATTORI, WASHIRA
TITLE OF INVENTION: NOVBL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 1
FEMALET OF THE STATE OF THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 1, Application US/10156761; Publication No. US20030119018A1; GENERAL INFORMATION:
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11.9%;
Best Local Similarity 48.4%;
Matches 411; Conservative
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LOCATION: (4187715)
OTHER INFORMATION: a, t, c,
US-10-156-761-1
                                                                                                                                                                                GAAGTTCGTG 900
                                                                                                                                                                                                                                                                                          GAÁGTTCCTG 921
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US-10-156-761-1/c
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Pred. No. 4.2e-25;
0; Mismatches 421; Indels
; CURRENT APPLICATION NUMBER: US/10/156,761
; CIRRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: UP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR APPLICATION NUMBER: JP 2001-272697
; NUMBER OF SEQ ID NOS: 15109
; LENGTH: 951
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Best Local Similarity 48.4%;
Matches 411; Conservative
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; NAME/KEY: CDS

; LOCATION: (1)..(951)

US-10-156-761-3347
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                                CCAGACGAATCAGCCGAGTGGAAAAACACGCAGGCACCCCACTTT
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APPLICANT: SHIBA, TADAYOSHI
APPLICANT: BARAKI, YOSHIYUKI
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-06-30
PRIOR FILING DATE: 2001-08-02
NUMBER: OF SEQ ID NOS: 15109
LENGTH: 936
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HORIKAWA, HIROSHI
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                                                  531 CCTAGCTGTTCCCGCAGATCACCGGCTTGCCTCCTTTTCTGGCCAAGGAGAATTGCCGTT
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                                                                                                                                              591 GATTACTGCGGGGAAGCCTTTCGTGGCGATGCGAGGTTTCGGCACCCCGACTCCT
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Pred. No. 3.5e-20;
0; Mismatches 382; Indels 15; Gaps
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; LOCATTON: (4187715)

; OTHER INFORMATION: a, t, c, g, other or unknown

US-10-156-761-1
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: ISHIKAWA, JUN
APPLICANT: SHIKAWA, HROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: HATTORI, WASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REPREMENCE: 249-262
CURRENT PILING DATE: 2002-05-29
PRIOR PILING DATE: 2001-05-30
PRIOR PLING DATE: 2001-05-30
PRIOR PLING DATE: 2001-05-30
PRIOR PLING DATE: 2001-06-30
PRIOR PLING DATE: 2001-06-30
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Publication No. US20030119018A1
GENERAL INFORMATION:
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: SHIRAWA, HROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SATAKI, YOSHIUVICI
APPLICANT: HATTORI, MASAHIRA
ITILE OF INVENTION: NOVEL POLYNUCLEOTIDES
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Publication No. US20030119018A1
GENERAL INFORMATION:
                                                                                                    10.5%;
                                                                                                                                         Best Local Similarity 47.7
Matches 362; Conservative
; LOCATION: (1)..(936)
US-10-156-761-1506
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44.7%; Pred. No. 2.1e-13;
tive 0; Mismatches 414;
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
; PRIOR FILING DATE: 2001-08-02
; RINDRER OF SEQ ID NOS: 15109
; LENGTH: 936
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APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIRAWA, JUN
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHARXI, YOSHIYUKI
APPLICANT: HATTORI, WASAHIRA
TITLE OF INVENITOR: 109-22
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT APPLICATION NUMBER: UP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 4980
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Pred. No. 2.2e-12;
0; Mismatches 406;
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CMURA, SATOSHI
APPLICANT: ISHIKAWA, JUN
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APPLICANT: SHIRAW, HROSHI
APPLICANT: SHIRAW, HROSHI
APPLICANT: SHIRAW, HROSHI
APPLICANT: SHIRAW, HORNERWA
ITTLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT PILING DATE: 2002-05-29
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-06-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 7265

LENGTH: 891
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Best Local Similarity 44.5%;
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46.0%; Pred. No. 1e-08;
ive 0; Mismatches 238;
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APPLICANT: ISHLKAWA, HIROSHI
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SAKAKI, YOSHIVUKI
APPLICANT: SAKAKI, YOSHIVUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT APPLICATION NUMBER: JP 2001-204089
PRIOR PLING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
NUMBER OF SEQ ID NOS: 15109
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Publication No. US20030119018A1
GENERAL INPORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: ISEBA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
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US-10-156-761-1152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               700
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ACCAAGCGGCAGCAATGCTCCTGGTAGATCGTGTTTTGGCTGATGAAACTGACCTCGCAT
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                                                                                   377 AGGAGGCCGAACCGCCCCCCCCCCCCAGATGCTGCCGCGAGGCCGACTGCGATGTGGCCC
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Pred. No. 9.2e-09;
0; Mismatches 216;
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: OWURA, SATOSHI
APPLICANT: ISHIKAWA, UUN
APPLICANT: ISHIKAWA, UUN
APPLICANT: SHIRAY, HAROOI
APPLICANT: SHIRAY, HAROSHI
APPLICANT: SHIRAY, HAROSHI
APPLICANT: SHIRAY, HAROSHI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-06-02
NUMBER: OF SEO ID NOS: 15109
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Best Local Similarity 46.8
Matches 190; Conservative
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; LOCATION: (1)..(1008)
US-10-156-761-3218
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US-10-156-761-3218
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LENGTH: 1008
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329 TGGGCACTTGGATGGTCCCCGAACTTATCCGAACATTCCGCGCCGAACACCCCCAACGTAG 388
                                                  302 TCGCCGGGGTGCATGTGGCCCGGCTGCTCGCGGTTCCGGCCGCACATCCGGATGTGG 361
                                                                                                  389 AATTCCAACTCCACCAAGCGGCAGCAATGCTCCTGGTAGATCGTGTTTTGGCTGATGAAA 448
                                                                                                                                                    362 AGATCCGGTTGCGCCAGGCGGCTCGGGTGCGCTGGCGAGGAAGTCGCCGCCGCGCGTC 421
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PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-23

PRIOR PILING DATE: 2000-05-26

PRIOR PLING DATE: 2000-09-06

PRIOR PILING DATE: 2000-09-09

PRIOR PILING DATE: 2000-09-09

PRIOR PILING DATE: 2000-10-23

PRIOR PLING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/253, 625

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-12-29

PRIOR PILING DATE: 2001-02-09

PRIOR PILING DATE: 2001-02-09

PRIOR PLING DATE: 2001-02-09

PRIOR PLING DATE: 2001-02-09

PRIOR PILING DATE: 2001-02-09

PRIOR PLING DATE: 2001-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TLE OF INVENTION: Identification of Essential Genes in Microorganisms
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Pred. No. 1.2e-08;
0; Mismatches 225; Indels
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 31440, Application US/10282122A
Publication No. US20040029129A1
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PRIOR FILING DATE: 2000-03-21
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APPLICANT: Wang, Liangsu
APPLICANT: Manio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Maselbeck, Robert
APPLICANT: Obleen, Kari
APPLICANT: Cyskind, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
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Best Local Similarity 46.4%;
Matches 195; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zyskind, Judith
Wall, Daniel
Trawick, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carr, Grant
                                                                                                                                                                                                                                                                                                                                                            -122A-31440
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